

# SEQUENCE LISTING

<110> GROGER, HARALD  
 WERNER, HELGE  
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 MENZEL, ANNE  
 HUMMEL, WERNER

<120> PROCESS FOR PREPARING OPTICALLY ACTIVE AMINO ACIDS USING A  
 WHOLE-CELL CATALYST

<130> 294227US-10757-9350-0-X PCT

<140> 10/593,567

<141> 2006-09-20

<150> PCT/EP2005/002933

<151> 2005-03-18

<150> DE 102004014280.7

<151> 2004-03-22

<160> 13

<170> PatentIn version 3.5

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<211> 47

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
 primer

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aaaaaactta agaaggagat atacatatga cattagaaat cttcgaa

47

<210> 2

<211> 32

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence: Synthetic  
 primer

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32

<210> 3

<211> 30

<212> DNA

<213> Artificial Sequence

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 <223> Description of Artificial Sequence: Synthetic primer

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<210> 4  
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 <223> Description of Artificial Sequence: Synthetic primer

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 <212> DNA  
 <213> Bacillus cereus

<220>  
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tat gat tat gag caa gta gta ttt tgt caa gat aaa gaa tct ggt tta 100  
 Tyr Asp Tyr Glu Gln Val Val Phe Cys Gln Asp Lys Glu Ser Gly Leu  
 15 20 25

aaa gca att att gca att cat gat aca aca ctt gga ccg gct ctt ggt 148  
 Lys Ala Ile Ile Ala Ile His Asp Thr Thr Leu Gly Pro Ala Leu Gly  
 30 35 40

gga aca aga atg tgg aca tat gat tct gaa gaa gcg gcg att gaa gat 196  
 Gly Thr Arg Met Trp Thr Tyr Asp Ser Glu Glu Ala Ala Ile Glu Asp  
 45 50 55

gca ttg cgt ctt gca aaa ggg atg aca tac aaa aac gca gca gct ggt 244  
 Ala Leu Arg Leu Ala Lys Gly Met Thr Tyr Lys Asn Ala Ala Ala Gly  
 60 65 70 75

tta aac tta ggt ggt gcg aaa aca gta att atc ggt gat cct cgt aaa 292  
 Leu Asn Leu Gly Gly Ala Lys Thr Val Ile Ile Gly Asp Pro Arg Lys  
 80 85 90

gat aag agc gaa gca atg ttc cgt gca cta gga cgt tat atc caa gga 340

Asp Lys Ser Glu Ala Met Phe Arg Ala Leu Gly Arg Tyr Ile Gln Gly	
95 100 105	
cta aac gga cgt tac att aca gct gaa gat gtt ggt aca aca gta gat	388
Leu Asn Gly Arg Tyr Ile Thr Ala Glu Asp Val Gly Thr Thr Val Asp	
110 115 120	
gat atg gat att atc cat gaa gaa act gac ttt gta aca ggt atc tca	436
Asp Met Asp Ile Ile His Glu Glu Thr Asp Phe Val Thr Gly Ile Ser	
125 130 135	
cca tca ttc ggt tct tct ggt aac cca tct ccg gta act gca tac ggt	484
Pro Ser Phe Gly Ser Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly	
140 145 150 155	
gtt tac cgt ggt atg aaa gca gct gca aaa gaa gct ttc ggt act gac	532
Val Tyr Arg Gly Met Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp	
160 165 170	
aat tta gaa gga aaa gta att gct gtt caa ggc gtt ggt aac gta gca	580
Asn Leu Glu Gly Lys Val Ile Ala Val Gln Gly Val Gly Asn Val Ala	
175 180 185	
tat cac cta tgc aaa cat tta cac gct gaa gga gca aaa tta att gtt	628
Tyr His Leu Cys Lys His Leu His Ala Glu Gly Ala Lys Leu Ile Val	
190 195 200	
aca gat att aat aaa gaa gct gta caa cgt gct gta gaa gaa ttc ggt	676
Thr Asp Ile Asn Lys Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly	
205 210 215	
gca tca gca gtt gaa cca aat gaa att tac ggt gtt gaa tgc gat att	724
Ala Ser Ala Val Glu Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile	
220 225 230 235	
tac gca cca tgt gca cta ggc gca aca gtt aat gat gaa act att cca	772
Tyr Ala Pro Cys Ala Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro	
240 245 250	
caa ctt aaa gca aaa gta atc gca ggt tct gcg aat aac caa tta aaa	820
Gln Leu Lys Ala Lys Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys	
255 260 265	
gaa gat cgt cat ggt gac atc att cat gaa atg ggt att gta tac gca	868
Glu Asp Arg His Gly Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala	
270 275 280	
cca gat tat gta att aat gca ggt ggc gta att aac gta gca gac gaa	916
Pro Asp Tyr Val Ile Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu	
285 290 295	
tta tat gga tac aat aga gaa cgt gca cta aaa cgt gtt gag tct att	964
Leu Tyr Gly Tyr Asn Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile	
300 305 310 315	
tat gac acg att gca aaa gta atc gaa att tca aaa cgc gat ggc ata	1012
Tyr Asp Thr Ile Ala Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile	

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gca act tat gta gcg gca gat cgt cta gct gaa gag cgc att gca agc				1060
Ala Thr Tyr Val Ala Ala Asp Arg Leu Ala Glu Glu Arg Ile Ala Ser				
	335	340	345	
ttg aag aat tct cgt agc act tac tta cgc aac ggt cac gat att att				1108
Leu Lys Asn Ser Arg Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile				
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Ser Arg Arg				
	365			

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 <213> Bacillus cereus

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Ile	His	Asp	Thr	Thr	Leu	Gly	Pro	Ala	Leu	Gly	Gly	Thr	Arg	Met	Trp
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Thr	Tyr	Asp	Ser	Glu	Glu	Ala	Ala	Ile	Glu	Asp	Ala	Leu	Arg	Leu	Ala
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Lys	Gly	Met	Thr	Tyr	Lys	Asn	Ala	Ala	Ala	Gly	Leu	Asn	Leu	Gly	Gly
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Ala	Lys	Thr	Val	Ile	Ile	Gly	Asp	Pro	Arg	Lys	Asp	Lys	Ser	Glu	Ala
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Met	Phe	Arg	Ala	Leu	Gly	Arg	Tyr	Ile	Gln	Gly	Leu	Asn	Gly	Arg	Tyr
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Ile	Thr	Ala	Glu	Asp	Val	Gly	Thr	Thr	Val	Asp	Asp	Met	Asp	Ile	Ile
		115					120					125			

His	Glu	Glu	Thr	Asp	Phe	Val	Thr	Gly	Ile	Ser	Pro	Ser	Phe	Gly	Ser
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Ser Gly Asn Pro Ser Pro Val Thr Ala Tyr Gly Val Tyr Arg Gly Met  
145 150 155 160

Lys Ala Ala Ala Lys Glu Ala Phe Gly Thr Asp Asn Leu Glu Gly Lys  
165 170 175

Val Ile Ala Val Gln Gly Val Gly Asn Val Ala Tyr His Leu Cys Lys  
180 185 190

His Leu His Ala Glu Gly Ala Lys Leu Ile Val Thr Asp Ile Asn Lys  
195 200 205

Glu Ala Val Gln Arg Ala Val Glu Glu Phe Gly Ala Ser Ala Val Glu  
210 215 220

Pro Asn Glu Ile Tyr Gly Val Glu Cys Asp Ile Tyr Ala Pro Cys Ala  
225 230 235 240

Leu Gly Ala Thr Val Asn Asp Glu Thr Ile Pro Gln Leu Lys Ala Lys  
245 250 255

Val Ile Ala Gly Ser Ala Asn Asn Gln Leu Lys Glu Asp Arg His Gly  
260 265 270

Asp Ile Ile His Glu Met Gly Ile Val Tyr Ala Pro Asp Tyr Val Ile  
275 280 285

Asn Ala Gly Gly Val Ile Asn Val Ala Asp Glu Leu Tyr Gly Tyr Asn  
290 295 300

Arg Glu Arg Ala Leu Lys Arg Val Glu Ser Ile Tyr Asp Thr Ile Ala  
305 310 315 320

Lys Val Ile Glu Ile Ser Lys Arg Asp Gly Ile Ala Thr Tyr Val Ala  
325 330 335

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340 345 350

Ser Thr Tyr Leu Arg Asn Gly His Asp Ile Ile Ser Arg Arg  
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<211> 1095  
 <212> DNA  
 <213> Candida boidinii

<220>  
 <221> CDS  
 <222> (1)..(1095)

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gaa gaa aaa tta tat ggt tct act gaa aat aaa tta ggt att gct aat 96  
 Glu Glu Lys Leu Tyr Gly Ser Thr Glu Asn Lys Leu Gly Ile Ala Asn  
 20 25 30

tgg tta aaa gat caa ggt cat gaa cta att act act tct gat aaa gaa 144  
 Trp Leu Lys Asp Gln Gly His Glu Leu Ile Thr Thr Ser Asp Lys Glu  
 35 40 45

ggt gaa aca agt gaa ttg gat aaa cat atc cca gat gct gat att atc 192  
 Gly Glu Thr Ser Glu Leu Asp Lys His Ile Pro Asp Ala Asp Ile Ile  
 50 55 60

atc acc act cct ttc cat cct gct tat atc act aag gaa aga ctt gac 240  
 Ile Thr Thr Pro Phe His Pro Ala Tyr Ile Thr Lys Glu Arg Leu Asp  
 65 70 75 80

aag gct aag aac tta aaa tta gtc gtt gtc gct ggt gtt ggt tct gat 288  
 Lys Ala Lys Asn Leu Lys Leu Val Val Val Ala Gly Val Gly Ser Asp  
 85 90 95

cac att gat tta gat tat att aat caa aca ggt aag aaa atc tca gtc 336  
 His Ile Asp Leu Asp Tyr Ile Asn Gln Thr Gly Lys Lys Ile Ser Val  
 100 105 110

ctg gaa gtt aca ggt tct aat gtt gtc tct gtt gct gaa cac gtt gtc 384  
 Leu Glu Val Thr Gly Ser Asn Val Val Ser Val Ala Glu His Val Val  
 115 120 125

atg acc atg ctt gtc ttg gtt aga aat ttc gtt cca gca cat gaa caa 432  
 Met Thr Met Leu Val Leu Val Arg Asn Phe Val Pro Ala His Glu Gln  
 130 135 140

att att aac cac gat tgg gag gtt gct gct atc gct aag gat gct tac 480  
 Ile Ile Asn His Asp Trp Glu Val Ala Ala Ile Ala Lys Asp Ala Tyr  
 145 150 155 160

gat atc gaa ggt aaa act atc gct acc att ggt gct ggt aga att ggt 528  
 Asp Ile Glu Gly Lys Thr Ile Ala Thr Ile Gly Ala Gly Arg Ile Gly  
 165 170 175

tac aga gtc ttg gaa aga tta ctc cca ttt aat cca aaa gaa tta tta 576  
 Tyr Arg Val Leu Glu Arg Leu Leu Pro Phe Asn Pro Lys Glu Leu Leu  
 180 185 190

tac tac gat tat caa gct tta cca aaa gaa gct gaa gaa aaa gtt ggt Tyr Tyr Asp Tyr Gln Ala Leu Pro Lys Glu Ala Glu Glu Lys Val Gly 195 200 205	624
gct aga aga gtt gaa aat att gaa gaa tta gtt gct caa gct gat atc Ala Arg Arg Val Glu Asn Ile Glu Glu Leu Val Ala Gln Ala Asp Ile 210 215 220	672
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ggt aaa ttt gat tac aga cca caa gat att atc tta tta aat ggt gaa Gly Lys Phe Asp Tyr Arg Pro Gln Asp Ile Ile Leu Leu Asn Gly Glu 340 345 350	1056
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 <213> *Candida boidinii*

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Gly	Glu	Thr	Ser	Glu	Leu	Asp	Lys	His	Ile	Pro	Asp	Ala	Asp	Ile	Ile		
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Ile	Thr	Thr	Pro	Phe	His	Pro	Ala	Tyr	Ile	Thr	Lys	Glu	Arg	Leu	Asp		
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Lys	Ala	Lys	Asn	Leu	Lys	Leu	Val	Val	Val	Ala	Gly	Val	Gly	Ser	Asp		
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His	Ile	Asp	Leu	Asp	Tyr	Ile	Asn	Gln	Thr	Gly	Lys	Lys	Ile	Ser	Val		
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Leu	Glu	Val	Thr	Gly	Ser	Asn	Val	Val	Ser	Val	Ala	Glu	His	Val	Val		
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Met	Thr	Met	Leu	Val	Leu	Val	Arg	Asn	Phe	Val	Pro	Ala	His	Glu	Gln		
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Tyr	Arg	Val	Leu	Glu	Arg	Leu	Leu	Pro	Phe	Asn	Pro	Lys	Glu	Leu	Leu		
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Tyr	Tyr	Asp	Tyr	Gln	Ala	Leu	Pro	Lys	Glu	Ala	Glu	Glu	Lys	Val	Gly		
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Ala	Arg	Arg	Val	Glu	Asn	Ile	Glu	Glu	Leu	Val	Ala	Gln	Ala	Asp	Ile		
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Val	Thr	Val	Asn	Ala	Pro	Leu	His	Ala	Gly	Thr	Lys	Gly	Leu	Ile	Asn		
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Lys	Glu	Leu	Leu	Ser	Lys	Phe	Lys	Lys	Gly	Ala	Trp	Leu	Val	Asn	Thr		
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Ala Arg Gly Ala Ile Ala Val Ala Glu Asp Val Ala Ala Ala Leu Glu  
260 265 270

Ser Gly Gln Leu Arg Gly Tyr Gly Gly Asp Val Trp Phe Pro Gln Pro  
275 280 285

Ala Pro Lys Asp His Pro Trp Arg Asp Met Arg Asn Lys Tyr Gly Ala  
290 295 300

Gly Asn Ala Met Thr Pro His Tyr Ser Gly Thr Thr Leu Asp Ala Gln  
305 310 315 320

Thr Arg Tyr Ala Glu Gly Thr Lys Asn Ile Leu Glu Ser Phe Phe Thr  
325 330 335

Gly Lys Phe Asp Tyr Arg Pro Gln Asp Ile Ile Leu Leu Asn Gly Glu  
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<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
Plasmid pAM3.25

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actaattact acttctgata aagaaggtga aacaagtga ttggataaac atatcccaga	180
tgctgatatt atcatcacca ctcttttcca tctgcttat atcactaagg aaagacttga	240
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Met Glu Pro Lys Thr Lys Lys Gln Arg Ser Leu Tyr Ile Pro Tyr Ala
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Gly Pro Val Leu Leu Glu Phe Pro Leu Leu Asn Lys Gly Ser Ala Phe
30             35             40

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gtg gtc gaa acc atc gaa gaa caa gcg gaa cga gca tgg atc cag tat 243
Val Val Glu Thr Ile Glu Glu Gln Ala Glu Arg Ala Trp Ile Gln Tyr
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Gln Gly Phe Lys Thr Glu Ile Asp Lys His Ile Tyr Leu Arg Asn Ile
75             80             85

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Gln Asp Thr Asn Glu Thr Leu Phe Tyr Arg Leu Val Asn Asn His Leu
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Pro Leu Leu Asn Lys Gly Ser Ala Phe Ser Met Glu Glu Arg Arg Asn
35          40          45

Phe Asn Leu Leu Gly Leu Leu Pro Glu Val Val Glu Thr Ile Glu Glu
50          55          60

Gln Ala Glu Arg Ala Trp Ile Gln Tyr Gln Gly Phe Lys Thr Glu Ile
65          70          75          80

Asp Lys His Ile Tyr Leu Arg Asn Ile Gln Asp Thr Asn Glu Thr Leu
85          90          95

Phe Tyr Arg Leu Val Asn Asn His Leu Asp Glu Met Met Pro Val Ile
100         105         110

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Tyr Thr Pro Thr Val Gly Ala Ala Cys Glu Arg Phe Ser Glu Ile Tyr  
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Arg Arg Ser Arg Gly Val Phe Ile Ser Tyr Gln Asn Arg His Asn Met  
130 135 140

Asp Asp Ile Leu Gln Asn Val Pro Asn His Asn Ile Lys Val Ile Val  
145 150 155 160

Val Thr Asp Gly Glu Arg Ile Leu Gly Leu Gly Asp Gln Gly Ile Gly  
165 170 175

Gly Met Gly Ile Pro Ile Gly Lys Leu Ser Leu Tyr Thr Ala Cys Gly  
180 185 190

Gly Ile Ser Pro Ala Tyr Thr Leu Pro Val Val Leu Asp Val Gly Thr  
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Asn Asn Gln Gln Leu Leu Asn Asp Pro Leu Tyr Met Gly Trp Arg Asn  
210 215 220

Pro Arg Ile Thr Asp Asp Glu Tyr Tyr Glu Phe Val Asp Glu Phe Ile  
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Gln Ala Val Lys Gln Arg Trp Pro Asp Val Leu Leu Gln Phe Glu Asp  
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Phe Ala Gln Lys Asn Ala Met Pro Leu Leu Asn Arg Tyr Arg Asn Glu  
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Ile Cys Ser Phe Asn Asp Asp Ile Gln Gly Thr Ala Ala Val Thr Val  
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Gly Thr Leu Ile Ala Ala Ser Arg Ala Ala Gly Gly Gln Leu Ser Glu  
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Lys Lys Ile Val Phe Leu Gly Ala Gly Ser Ala Gly Cys Gly Ile Ala  
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Glu Met Ile Ile Ser Gln Thr Gln Arg Glu Gly Leu Ser Glu Glu Ala  
325 330 335

Ala Arg Gln Lys Val Phe Met Val Asp Arg Phe Gly Leu Leu Thr Asp  
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Lys Met Pro Asn Leu Leu Pro Phe Gln Thr Lys Leu Val Gln Lys Arg  
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Glu Asn Leu Ser Asp Trp Asp Thr Asp Ser Asp Val Leu Ser Leu Leu  
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Asp Val Val Arg Asn Val Lys Pro Asp Ile Leu Ile Gly Val Ser Gly  
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Gln Thr Gly Leu Phe Thr Glu Glu Ile Ile Arg Glu Met His Lys His  
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Cys Pro Arg Pro Ile Val Met Pro Leu Ser Asn Pro Thr Ser Arg Val  
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Glu Ala Thr Pro Gln Asp Ile Ile Ala Trp Thr Glu Gly Asn Ala Leu  
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Val Ala Thr Gly Ser Pro Phe Asn Pro Val Val Trp Lys Asp Lys Ile  
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Tyr Pro Ile Ala Gln Cys Asn Asn Ala Phe Ile Phe Pro Gly Ile Gly  
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Leu Gly Val Ile Ala Ser Gly Ala Ser Arg Ile Thr Asp Glu Met Leu  
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Met Ser Ala Ser Glu Thr Leu Ala Gln Tyr Ser Pro Leu Val Leu Asn  
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Gly Glu Gly Met Val Leu Pro Glu Leu Lys Asp Ile Gln Lys Val Ser  
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Arg Ala Ile Ala Phe Ala Val Gly Lys Met Ala Gln Gln Gln Gly Val  
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